What is claimed is:

1. A method for obtaining genetic information from a biological sample potentially comprising target nucleic acid molecules, said method comprising the steps of:

   a) providing nucleic acid molecules that are (i) target nucleic acid molecules in said sample, or (ii) probes that hybridize to target nucleic acid molecules in said sample, or (iii) amplification products of (i) or (ii), or (iv) a genomic representation of (i); and

   b) detecting target nucleic acid molecules by contacting or comparing the nucleic acid molecules of (a) with a detection ensemble that has a minimum genomic derivation of greater than five and that comprises detection sequences that can detect target nucleic acid molecules.

2. The method of claim 1, further comprising the step of (c) identifying nucleic acid molecules detected in step (b).

3. The method of claim 1, wherein the detection ensemble has a minimum genomic derivation of greater than 11.

4. The method of claim 1, wherein the nucleic acid molecules of step (a) are not immobilized as size fractionated fragments in a matrix or on a solid support.

5. The method of claim 1, further comprising using fewer than four pairs of amplification sequences, to yield, if target nucleic acid molecules are present in the sample, amplification products.

6. The method of claim 5, wherein amplification is carried out using a single pair of amplification sequences.

7. The method of claim 1, wherein said method is used to quantify a target organism in said biological sample by *in situ* hybridization.

8. The method of claim 1, wherein prior to step (a), nucleic acid molecules of said sample are hybridized, simultaneously, with an ensemble of ID probes to yield the probes of step (a)(ii).

9. The method of claim 1, wherein the probes of step (a)(ii) include (i) a first region capable of hybridizing to a target nucleic acid molecule, and (ii) amplification sequences.

10. The method of claim 1, wherein said nucleic acid molecules of said sample are fixed to a solid support.

11. The method of claim 1, wherein said nucleic acid molecules of step (a) are in the liquid phase.

12. The method of claim 1, wherein at least some of the nucleic acid molecules of step (a) comprise one or more oligonucleotide tags.

13. The method of claim 1, wherein at least some of the probes of step (a)(ii) comprise: (i) two or more oligonucleotides that can be ligated to one another upon hybridization to a target nucleic acid molecule, and (ii) amplification sequences.

14. The method of claim 1, wherein said detection sequences of said detection ensemble are arrayed as spots in two dimensions or as parallel stripes on a solid support.

15. The method of claim 8, wherein said ensemble of ID probes includes probes that hybridize to at least two different nucleic acid molecules from each of at least ten different viruses, each of which belongs to a different genus.

16. The method of claim 1, wherein said biological sample is a gastrointestinal tract sample, and said genetic information is the identification of nucleic acid molecules in said sample from 6 or more of *Escherichia coli*, Salmonella, Shigella, *Yersinia enterocolitica*, *Vibrio cholera*, *Campylobacter fecalis*, *Clostridium difficile*, Rotavirus, Norwalk virus, Astrovirus, Adenovirus, Coronavirus, *Giardia lamblia*, *Entamoeba histolytica*, *Blastocystis hominis*, Cryptosporidium, Microsporidium, *Necator americanus*, *Ascaris lumbricoides*, *Trichuris trichiura*, *Enterobius vermicularis*, *Strongyloides stercoralis*, *Opsthorchis viverrini*, *Clonorchis sinensis*, and *Hymenoplepis nana*.

17. The method of claim 1, wherein said biological sample is a respiratory tract sample, and said genetic information is the identification of nucleic acid molecules in said sample from 6 or more of *Cornybacterium diphtheriae*, *Mycobacterium tuberculosis*, *Mycoplasma pneumoniae*, *Chlamydia trachomatis*, *Chlamydia pneumoniae*, *Bordetella pertussis*, Legionella spp., Nocardia spp., *Streptococcus pneumoniae*, *Haemophilus influenzae*, *Chlamydia psittaci*, *Pseudomonas aeruginosa*, *Staphylococcus aureus*, *Histoplasma capsulatum*, *Coccidoides immitis*, *Cryptococcus neoformans*, *Blastomyces*

dermatitidis, *Pneumocystis carinii*, Respiratory Syncytial Virus, Adenovirus, Herpes simplex virus, Influenza virus, Parainfluenza virus, and Rhinovirus.

18. The method of claim 1, wherein said biological sample is a blood sample, and said genetic information is the identification of nucleic acid molecules in said sample from 6 or more of Coagulase-negative *staphylococci*, *Staphylococcus aureus*, *Viridans streptococci*, Enterococcus spp., Beta-hemolytic streptococci, *Streptococcus pneumoniae*, Escherichia spp., Klebsiella spp., Pseudomonas spp., Enterbater spp., Proteus spp., Bacteroides spp., Clostridium spp., *Pseudomonas aueruginosa*, Cornybacterium spp., Plasmodium spp., *Leishmania donovani*, Toxoplasma spp., Microfilariae, Fungi, *Histoplasma capsulatum*, *Coccidoides immitis*, *Cryptococcus neoformans*, Candida spp., HIV, Herpes simplex virus, Hepatitis C virus, Hepatitis B virus, Cytomegalovirus, and Epstein-Barr virus.

19. The method of claim 1, wherein said genetic information is the identification of nucleic acid molecules in said sample from 6 or more of coxsakievirus A, Herpes simplex virus, St. Louis encephalitis virus, Epstein-Barr virus, myxovirus, JC virus, coxsakievirus B, togavirus, measles virus, a hepatitis virus, paramyxovirus, echovirus, bunyavirus, cytomegalovirus, varicella-zoster virus, HIV, mumps virus, equine encephalitis virus, lymphocytic choriomeningitis virus, rabies virus, and BK virus.

20. The method of claim 8, wherein at least 50% of the probes comprising said ensemble of nucleic acid probes are capable of hybridizing to pre-determined

genomic difference sequences that are potentially present in said sample or in a genomic representation of said sample.

21. A kit for obtaining genetic information from a biological sample, comprising:

    a) a plurality of ID probes and/or SNP probes; and

    b) a detection ensemble comprising detection sequences that are congruent with probes of (a), wherein said detection ensemble has a minimum genomic derivation of greater than five.

22. The kit of claim 21, wherein (a) comprises more than ten different amplifiable probes.

23. The kit of claim 22, wherein (a) comprises more than fifty different amplifiable probes.

24. The kit of claim 23, wherein (a) comprises more than two hundred and fifty different amplifiable probes.

25. The kit of claim 21, wherein the detection ensemble has a minimum genomic derivation of greater than 11.

26. The kit of claim 21, wherein (a) comprises more than five families of amplifiable probes.

27. The kit of claim 21, wherein the probes of (a) are specific for at least two distinct taxa.

28. The kit of claim 27, wherein the probes of (a) are specific for at least two different species.

29. The kit of claim 27, wherein the probes of (a) are specific for at least two different genera.

30. The kit of claim 27, wherein the probes of (a) are specific for at least two different kingdoms.

31. The kit of claim 21, wherein the probes of (a) include probes that comprise: (i) two or more oligonucleotides that can be ligated to one another upon hybridization to an ID sequence of a target nucleic acid molecules, and (ii) amplification sequences.

32. The kit of claim 21, wherein the probes of (a) and/or the detection sequences of (b) are physically attached to distinct locations on a solid support.

33. The kit of claim 21, wherein at least 50% of the probes of (a) comprise genomic difference sequences from at least three different species.

34. The kit of claim 32, in which the detection sequences comprised by the detection ensemble that detect (i) members of a taxonomic group and (ii) closely related taxonomic groups are positioned adjacent to one another on said support.

35. An ensemble of ID probes that can be amplified using fewer than four pairs of amplification sequences and that comprises more than three families of ID probes and more than ten different ID probes.

36. The ensemble of claim 35, comprising more than fifty different amplifiable ID probes.

37. The ensemble of claim 36, comprising more than two hundred and fifty different amplifiable ID probes.

38. The ensemble of claim 35, comprising more than ten families of amplifiable ID probes.

39. The ensemble of claim 35, comprising more than twenty-five families of amplifiable ID probes.

40. The ensemble of claim 35, wherein more than two of said families of amplifiable probes are specific for non-overlapping taxa.

41. The ensemble of claim 35, wherein more than two of said families of amplifiable probes are specific for different species.

42. The ensemble of claim 35, wherein more than two of said families of amplifiable probes are specific for different genera.

43. The ensemble of claim 35, wherein more than two of said families of amplifiable probes are specific for different kingdoms.

44. The ensemble of claim 35, wherein the probes of (a) include probes that comprise: (i) two or more oligonucleotides that can be ligated to one another upon hybridization to an ID sequence of a target nucleic acid molecule, and (ii) amplification sequences.

45. The ensemble of claim 35, wherein at least 50% of said probes comprise genomic difference sequences from at least three different species.

46. The ensemble of claim 35, in which the detection sequences comprised by the detection ensemble that detect (i) members of a taxonomic group and (ii) closely related taxonomic groups are positioned adjacent to one another on a support.

47. A method for obtaining genetic information from a biological sample potentially comprising target nucleic acid molecules, said method comprising the steps of:

a) providing an ensemble of nucleic acid probes having a minimum genomic derivation of greater than five;

b) contacting said ensemble of probes, simultaneously, with nucleic acid molecules of said sample;

c) detecting hybridization between said probes and any target nucleic acid molecules of said sample; and

d) identifying nucleic acid molecules detected in step (c).

48. The method of claim 13, wherein said oligonucleotides that can be ligated are SNP probes.

49. The method of claim 48, wherein at least some of said SNP probes comprise tag sequences that can hybridize to tag sequences in a detection ensemble comprising an ensemble of tag sequences congruent to said SNP probes.

50. The method of claim 48, wherein the detection ensemble has a minimum genomic derivation of greater than 20.

51. The method claim 50, wherein the detection ensemble has a minimum genomic variation of greater than 50.

52. The method of claim 1, wherein the amplification products of step (a)(iv) are generated by amplification of target nucleic acid molecules of step (a)(i) using no more than four pairs of amplification sequences.

53. The method of claim 52, wherein said amplification sequences direct the amplification of sequences lying between Alu repeats using Alu-specific primers.

54. The method of claim 52, wherein the detection ensemble of (b) comprises ID sites that are congruent to ID probes potentially amplified in step (a)(iv).

55. A kit for obtaining genetic information from a biological sample, comprising

a) a plurality of nucleic acid primers that are capable of priming the amplification of DNA sequences flanked by repetitive sequences in target genomic DNA in a biological sample to yield ID probes; and

b) a detection ensemble comprising detection sequences that are congruent with ID probes potentially amplified using the primers of (a), wherein said detection ensemble has a minimum genomic derivation of greater than five.

56. The kit of claim 55, wherein said detection ensemble has a minimum genomic derivation of greater than 20.

57. The kit of claim 55, wherein said repetitive sequences are human Alu repeats, and said primers are Alu-specific primers.

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